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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/851,595

DATE: 05/21/2001
TIME: 10:17:13

P.S

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\05212001\I851595.raw

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 3 <110> APPLICANT: Gu, Wei
 5 <120> TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTORS AND USES THEREFOR
 7 <130> FILE REFERENCE: MNI-080CP
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/851,595
C--> 10 <141> CURRENT FILING DATE: 2001-05-08
12 <150> PRIOR APPLICATION NUMBER: 09/556,588
13 <151> PRIOR FILING DATE: 2000-05-08
15 <150> PRIOR APPLICATION NUMBER: 60/132,896
16 <151> PRIOR FILING DATE: 1999-05-06
18 <160> NUMBER OF SEQ ID NOS: 12
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3637
24 <212> TYPE: DNA
25 <213> ORGANISM: Mus musculus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (222)..(3122)
31 <220> FEATURE:
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (3554)
34 <223> OTHER INFORMATION: n = any nucleotide
36 <400> SEQUENCE: 1
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39 ccgctgccgc cgccgcgccc aagccaagtc gagcggggc gttgcccacc gacggcacag 120
41 ccccttgggcc cgcccgggac caggaggtga gccgcgcgcg cacagctccg tgcgctcgcc 180
43 cgtctgagcg cccgccaggt gccccgcagc ccgccgccga g atg cac agc ccg cct 236
                                                  Met His Ser Pro Pro
44                                                  1               5
45
47 ggg ctc ctg gcg ctg tgg ctt tgc gct gtg ctg tgc gca tcg gcg cgc 284
48 Gly Leu Leu Ala Leu Trp Leu Cys Ala Val Leu Cys Ala Ser Ala Arg
49                  10                  15                  20
51 ggg ggc agc gac ccc cag cct ggc ccg ggg cgt ccc gcc tgc ccg gct 332
52 Gly Gly Ser Asp Pro Gln Pro Gly Pro Gly Arg Pro Ala Cys Pro Ala
53                  25                  30                  35
55 ccc tgc cac tgc cag gag gac ggc atc atg ctg tcc gct gac tgc tcc 380
56 Pro Cys His Cys Gln Glu Asp Gly Ile Met Leu Ser Ala Asp Cys Ser
57                  40                  45                  50
59 gag ctc ggg ctc tca gtg gtg cct gcg gac ctg gac ccc ctg acg gct 428
60 Glu Leu Gly Leu Ser Val Val Pro Ala Asp Leu Asp Pro Leu Thr Ala
61          55                  60                  65
63 tac cta gac ctc agt atg aac aac ctc acg gag ctt cag ccg ggt ctc 476
64 Tyr Leu Asp Leu Ser Met Asn Asn Leu Thr Glu Leu Gln Pro Gly Leu
65 70                  75                  80                  85
67 ttc cac cac ctg cgc ttc ctg gag gag ctg cgg ctc tca ggg aac cac 524
68 Phe His His Leu Arg Phe Leu Glu Glu Leu Arg Leu Ser Gly Asn His
69                  90                  95                  100
```

ENTERED

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71 ctc tca cac atc ccg gga cag gca ttc tcc ggc ctc cac agc ctc aaa   572
72 Leu Ser His Ile Pro Gly Gln Ala Phe Ser Gly Leu His Ser Leu Lys
73            105               110               115
75 att cta atg ctg cag agc aac cag ctc cgt ggg atc cca gca gag gca   620
76 Ile Leu Met Leu Gln Ser Asn Gln Leu Arg Gly Ile Pro Ala Glu Ala
77            120               125               130
79 cta tgg gag ctg ccc agc ctg cag tcg ctg cgc cta gat gct aat ctc   668
80 Leu Trp Glu Leu Pro Ser Leu Gln Ser Leu Arg Leu Asp Ala Asn Leu
81       135               140               145
83 atc tcc ctg gtc cct gag aga agc ttt gag ggg ctc tcc tcc ctc cgc   716
84 Ile Ser Leu Val Pro Glu Arg Ser Phe Glu Gly Leu Ser Ser Leu Arg
85 150               155               160               165
87 cac ctc tgg ctg gat gac aat gca ctc act gag atc ccc gtc aga gct   764
88 His Leu Trp Leu Asp Asp Asn Ala Leu Thr Glu Ile Pro Val Arg Ala
89            170               175               180
91 ctc aac aac ctt cct gcc cta cag gcc atg acc ttg gct ctc aac cat   812
92 Leu Asn Asn Leu Pro Ala Leu Gln Ala Met Thr Leu Ala Leu Asn His
93            185               190               195
95 atc cgc cac atc cct gac tat gcc ttc cag aac ctc acc agt ctt gtg   860
96 Ile Arg His Ile Pro Asp Tyr Ala Phe Gln Asn Leu Thr Ser Leu Val
97       200               205               210
99 gtg ctg cat cta cat aac aac cgc atc cag cat gtg ggg acc cac agc   908
100 Val Leu His Leu His Asn Asn Arg Ile Gln His Val Gly Thr His Ser
101      215               220               225
103 ttc gag ggg ctg cac aat ctg gag aca cta gac ctg aac tat aat gag   956
104 Phe Glu Gly Leu His Asn Leu Glu Thr Leu Asp Leu Asn Tyr Asn Glu
105 230               235               240               245
107 ctg cag gag ttc ccc ttg gct atc cgg acc ctg ggc agg ctg cag gaa   1004
108 Leu Gln Glu Phe Pro Leu Ala Ile Arg Thr Leu Gly Arg Leu Gln Glu
109            250               255               260
111 ttg ggt ttc cat aac aac aac atc aag gct atc cca gag aaa gcc ttc   1052
112 Leu Gly Phe His Asn Asn Asn Ile Lys Ala Ile Pro Glu Lys Ala Phe
113            265               270               275
115 atg ggc aac cct ctc ctg cag aca ata cat ttt tat gac aac cca atc   1100
116 Met Gly Asn Pro Leu Leu Gln Thr Ile His Phe Tyr Asp Asn Pro Ile
117      280               285               290
119 cag ttt gtg gga agg tca gca ttc cag tac ctg tct aaa ctg cat acg   1148
120 Gln Phe Val Gly Arg Ser Ala Phe Gln Tyr Leu Ser Lys Leu His Thr
121      295               300               305
123 cta tct ttg aat ggt gcc act gat atc caa gag ttc cca gac ctc aaa   1196
124 Leu Ser Leu Asn Gly Ala Thr Asp Ile Gln Glu Phe Pro Asp Leu Lys
125 310               315               320               325
127 ggc acc act agc ctg gag atc ctg acc ctg acc cgt gcg ggc atc aga   1244
128 Gly Thr Thr Ser Leu Glu Ile Leu Thr Leu Thr Arg Ala Gly Ile Arg
129            330               335               340
131 ctg ctc cca ccg gga gtg tgc caa cag ctg cct agg ctc cga atc ctg   1292
132 Leu Leu Pro Pro Gly Val Cys Gln Gln Leu Pro Arg Leu Arg Ile Leu
133            345               350               355
135 gag ctg tct cat aat cag atc gag gag tta ccc agc ctg cac aga tgt   1340
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136 Glu Leu Ser His Asn Gln Ile Glu Glu Leu Pro Ser Leu His Arg Cys
137       360                     365                 370
139 cag aag ctg gag gaa att ggc ctc cga cat aac agg atc aag gaa att   1388
140 Gln Lys Leu Glu Glu Ile Gly Leu Arg His Asn Arg Ile Lys Glu Ile
141       375                     380                 385
143 ggt gca gat acc ttc agc cag ctg ggc tcc ttg caa gct tta gac ctg   1436
144 Gly Ala Asp Thr Phe Ser Gln Leu Gly Ser Leu Gln Ala Leu Asp Leu
145 390                     395                 400                 405
147 agt tgg aat gcc atc cgt gcc atc cac cct gag gct ttc tca acc ctt   1484
148 Ser Trp Asn Ala Ile Arg Ala Ile His Pro Glu Ala Phe Ser Thr Leu
149                 410                     415                 420
151 cga tcc ttg gtt aag ctg gac ctg act gac aac cag ctg acc aca ctg   1532
152 Arg Ser Leu Val Lys Leu Asp Leu Thr Asp Asn Gln Leu Thr Thr Leu
153       425                     430                     435
155 ccc ctg gct ggg ctg gga ggc ctg atg cac ctg aag ctc aaa ggg aac   1580
156 Pro Leu Ala Gly Leu Gly Gly Leu Met His Leu Lys Leu Lys Gly Asn
157             440                     445                 450
159 ttg gcc ctg tct cag gcc ttc tcc aag gac agt ttc cca aaa ctg agg   1628
160 Leu Ala Leu Ser Gln Ala Phe Ser Lys Asp Ser Phe Pro Lys Leu Arg
161       455                     460                     465
163 atc ctg gag gtg ccc tac gcc tac cag tgc tgt gcc tac ggc atc tgt   1676
164 Ile Leu Glu Val Pro Tyr Ala Tyr Gln Cys Cys Ala Tyr Gly Ile Cys
165 470                     475                     480                 485
167 gcc agc ttc ttc aag acc tct ggg cag tgg cag gcc gag gac ttt cat   1724
168 Ala Ser Phe Phe Lys Thr Ser Gly Gln Trp Gln Ala Glu Asp Phe His
169                 490                     495                 500
171 cca gaa gaa gag gag gca cca aag agg ccc ctg ggt ctc ctt gct gga   1772
172 Pro Glu Glu Glu Glu Ala Pro Lys Arg Pro Leu Gly Leu Leu Ala Gly
173             505                     510                 515
175 caa gct gag aac cac tat gac cta gac ctg gat gag ctc cag atg ggg   1820
176 Gln Ala Glu Asn His Tyr Asp Leu Asp Leu Asp Glu Leu Gln Met Gly
177             520                     525                 530
179 aca gag gac tca aag cca aac ccc agt gtc cag tgc agc cct gtt cca   1868
180 Thr Glu Asp Ser Lys Pro Asn Pro Ser Val Gln Cys Ser Pro Val Pro
181       535                     540                 545
183 ggc ccc ttc aag ccc tgc gag cac ctc ttt gag agc tgg ggc atc cgc   1916
184 Gly Pro Phe Lys Pro Cys Glu His Leu Phe Glu Ser Trp Gly Ile Arg
185 550                     555                 560                 565
187 ctt gct gtg tgg gcc atc gtg ctg ctc tcc gta ctc tgt aac ggg ctg   1964
188 Leu Ala Val Trp Ala Ile Val Leu Leu Ser Val Leu Cys Asn Gly Leu
189             570                     575                 580
191 gtg ctg ctg aca gtc ttt gcc agc gga ccc agc ccg ctg tcc ccc gtc   2012
192 Val Leu Leu Thr Val Phe Ala Ser Gly Pro Ser Pro Leu Ser Pro Val
193             585                     590                 595
195 aag ctt gtg gtg ggt gcg atg gca ggc gcc aac gcc ctg acg ggc att   2060
196 Lys Leu Val Val Gly Ala Met Ala Gly Ala Asn Ala Leu Thr Gly Ile
197       600                     605                     610
199 tcc tgt ggt ctc ctg gcc tct gtg gac gcc ttg acc tat ggt cag ttc   2108
200 Ser Cys Gly Leu Leu Ala Ser Val Asp Ala Leu Thr Tyr Gly Gln Phe
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201      615                      620                 625
203 gct gag tat gga gcc cgc tgg gag agc ggt ctg ggc tgc cag gct acg   2156
204 Ala Glu Tyr Gly Ala Arg Trp Glu Ser Gly Leu Gly Cys Gln Ala Thr
205 630                  635                 640                 645
207 ggc ttc ctg gct gtc ctg ggt tca gag gcg tcg gtg ctg ctg ctc aca   2204
208 Gly Phe Leu Ala Val Leu Gly Ser Glu Ala Ser Val Leu Leu Leu Thr
209                  650                 655                 660
211 ctg gcg gcc gtg cag tgc agc atc tct gtg acc tgc gtc cga gcc tac   2252
212 Leu Ala Ala Val Gln Cys Ser Ile Ser Val Thr Cys Val Arg Ala Tyr
213              665                 670                 675
215 ggg aag gcg ccg tcg cct ggc agc gtc cgc gca ggc gca ctg gga tgc   2300
216 Gly Lys Ala Pro Ser Pro Gly Ser Val Arg Ala Gly Ala Leu Gly Cys
217          680                 685                 690
219 ctg gcg ctg gcc ggg ctg gcc gca gca ctg ccg ctg gcc tcg gtg gga   2348
220 Leu Ala Leu Ala Gly Leu Ala Ala Ala Leu Pro Leu Ala Ser Val Gly
221      695                 700                 705
223 gag tat ggc gcc tcc cca ctc tgc ctg ccc tac gcc cca ccc gag ggc   2396
224 Glu Tyr Gly Ala Ser Pro Leu Cys Leu Pro Tyr Ala Pro Pro Glu Gly
225 710                  715                 720                 725
227 cgg ccg gcc gcc ctg ggc ttc gct gta gcc ctg gtg atg atg aac tcg   2444
228 Arg Pro Ala Ala Leu Gly Phe Ala Val Ala Leu Val Met Met Asn Ser
229                  730                 735                 740
231 ctc tgc ttc ctg gtg gtg gcc ggc gcc tac atc aag ctc tac tgt gac   2492
232 Leu Cys Phe Leu Val Val Ala Gly Ala Tyr Ile Lys Leu Tyr Cys Asp
233              745                 750                 755
235 ctg cca cgg ggt gac ttt gag gcc gtg tgg gac tgc gcc atg gtg cgc   2540
236 Leu Pro Arg Gly Asp Phe Glu Ala Val Trp Asp Cys Ala Met Val Arg
237          760                 765                 770
239 cac gtg gcc tgg ctc atc ttt gca gat ggc ctc ctc tac tgc ccc gtg   2588
240 His Val Ala Trp Leu Ile Phe Ala Asp Gly Leu Leu Tyr Cys Pro Val
241      775 ·                 780                 785
243 gcc ttc ctc agc ttt gcc tcc atg ctg ggc ctc ttc cct gtc acc ccc   2636
244 Ala Phe Leu Ser Phe Ala Ser Met Leu Gly Leu Phe Pro Val Thr Pro
245 790                  795                 800                 805
247 gag gct gtc aag tca gtc ctt ctg gtg gtg ctg cct ctg cct gcc tgc   2684
248 Glu Ala Val Lys Ser Val Leu Leu Val Val Leu Pro Leu Pro Ala Cys
249                  810                 815                 820
251 ctc aac cca ctg ctc tac ctg ctc ttc aac cct cac ttc cgg gat gac   2732
252 Leu Asn Pro Leu Leu Tyr Leu Leu Phe Asn Pro His Phe Arg Asp Asp
253              825                 830                 835
255 ctt cgg cgg ctc tgg cca agc cct cgg tcc cca ggg ccc cta gcc tac   2780
256 Leu Arg Arg Leu Trp Pro Ser Pro Arg Ser Pro Gly Pro Leu Ala Tyr
257          840                 845                 850
259 gct gca gcc ggt gag ctg gag aag agc tcc tgc gac tcc acc caa gcg   2828
260 Ala Ala Ala Gly Glu Leu Glu Lys Ser Ser Cys Asp Ser Thr Gln Ala
261      855                 860                 865
263 ctg gtg gct ttc tca gat gtg gat ctt att ctg gaa gct tct gag gct   2876
264 Leu Val Ala Phe Ser Asp Val Asp Leu Ile Leu Glu Ala Ser Glu Ala
265 870                  875                 880                 885
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267 ggg cag cct cct ggg cta gag acc tat ggc ttc cct tca gtg acc ctc    2924
268 Gly Gln Pro Pro Gly Leu Glu Thr Tyr Gly Phe Pro Ser Val Thr Leu
269           890                   895                   900
271 atc tcc cga cat cag ccg ggg gcc acc agg ctg gag gga aac cat ttt    2972
272 Ile Ser Arg His Gln Pro Gly Ala Thr Arg Leu Glu Gly Asn His Phe
273           905                   910                   915
275 ata gag tct gat gga acc aag ttt ggg aac cca caa cct ccc atg aag    3020
276 Ile Glu Ser Asp Gly Thr Lys Phe Gly Asn Pro Gln Pro Pro Met Lys
277           920                   925               930
279 gga gaa ctg ctg ctg aag gca gag gga gcc act ttg gca ggc tgt ggc    3068
280 Gly Glu Leu Leu Leu Lys Ala Glu Gly Ala Thr Leu Ala Gly Cys Gly
281    935                   940               945
283 tct tcc gtg ggt gga gcc ctc tgg ccc tct ggc tct ctc ttt gcc tct    3116
284 Ser Ser Val Gly Gly Ala Leu Trp Pro Ser Gly Ser Leu Phe Ala Ser
285 950                   955               960               965
287 cac ttg taaatatccc tctctgtttg tcctctcccc atccaatgat ggctgcttat    3172
288 His Leu
290 aaaagaaaga caactccaac tccatagcaa gatggccaac acctctgact ccattgttct  3232
292 ctctccacga cccctaacca atgagtgctt ccaagtcttg ctttgtcttg gccttcagct  3292
294 tcactttcac cctgggcctt ctctgtccaa tccaatactt ctgacagagg cctgggaaat  3352
296 ttgcatagga gaaaggagaa aagcaaaaga cagtgaaggt tattgggccc tgacagagcc  3412
298 atgatcagta agtgcagagt gatggggagg tctcacagag catgacactg gaagacaact  3472
300 accaaagaca ttggagagtc tcccctgtga catatagaat ataaaatgtg ttctgcgttc  3532
W--> 302 cattaatctt gacctatgct gngccaaagt gcttcctgtt aaaatacact ttggaagaca 3592
304 ttgaaaaaaa aaaaaaaaaa aaaaaaaaa aaaagggcg gccgc                     3637
307 <210> SEQ ID NO: 2
308 <211> LENGTH: 967
309 <212> TYPE: PRT
310 <213> ORGANISM: Mus musculus
312 <400> SEQUENCE: 2
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317           20                  25                  30
319 Pro Ala Cys Pro Ala Pro Cys His Cys Gln Glu Asp Gly Ile Met Leu
320           35                  40                  45
322 Ser Ala Asp Cys Ser Glu Leu Gly Leu Ser Val Val Pro Ala Asp Leu
323  50                   55                  60
325 Asp Pro Leu Thr Ala Tyr Leu Asp Leu Ser Met Asn Asn Leu Thr Glu
326 65                   70                  75                  80
328 Leu Gln Pro Gly Leu Phe His His Leu Arg Phe Leu Glu Glu Leu Arg
329                   85                  90                  95
331 Leu Ser Gly Asn His Leu Ser His Ile Pro Gly Gln Ala Phe Ser Gly
332           100                 105                 110
334 Leu His Ser Leu Lys Ile Leu Met Leu Gln Ser Asn Gln Leu Arg Gly
335           115                 120                 125
337 Ile Pro Ala Glu Ala Leu Trp Glu Leu Pro Ser Leu Gln Ser Leu Arg
338           130                 135                 140
340 Leu Asp Ala Asn Leu Ile Ser Leu Val Pro Glu Arg Ser Phe Glu Gly
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6